

seqlist_12_20_06.txt

SEQUENCE LISTING

<110> Dale Umetsu
Rosemarie DeKruyff
Jennifer McIntire
Gordon Freeman

<120> T CELL REGULATORY GENES ASSOCIATED WITH
IMMUNE DISEASE

<130> STAN-235CIP

<150> 60/302,344
<151> 2001-06-29

<150> 10/188,012
<151> 2002-07-01

<160> 58

<170> FastSEQ for Windows Version 4.0

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<213> M. musculus

<220>
<221> VARIANT
<222> (1)...(305)
<223> TIM-1 BALB/c allele

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35 40 45
Cys Trp Gly Arg Gly Gln Cys Pro Ser Ser Ala Cys Gln Asn Thr Leu
50 55 60
Ile Trp Thr Asn Gly His Arg Val Thr Tyr Gln Lys Ser Ser Arg Tyr
65 70 75 80
Asn Leu Lys Gly His Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu
85 90 95
Asn Ser Val Glu Ser Asp Ser Gly Leu Tyr Cys Cys Arg Val Glu Ile
100 105 110
Pro Gly Trp Phe Asn Asp Gln Lys Val Thr Phe Ser Leu Gln Val Lys
115 120 125
Pro Glu Ile Pro Thr Arg Pro Pro Thr Arg Pro Thr Thr Thr Arg Pro
130 135 140
Thr Ala Thr Gly Arg Pro Thr Thr Ile Ser Thr Arg Ser Thr His Val
145 150 155 160
Pro Thr Ser Ile Arg Val Ser Thr Ser Thr Pro Pro Thr Ser Thr His
165 170 175
Thr Trp Thr His Lys Pro Glu Pro Thr Thr Phe Cys Pro His Glu Thr
180 185 190
Thr Ala Glu Val Thr Gly Ile Pro Ser His Thr Pro Thr Asp Trp Asn
195 200 205
Gly Thr Val Thr Ser Ser Gly Asp Thr Trp Ser Asn His Thr Glu Ala
210 215 220
Ile Pro Pro Gly Lys Pro Gln Lys Asn Pro Thr Lys Gly Phe Tyr Val

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225	230	235	240
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245	250	255	
Ala Ile Thr Arg Tyr Ile Leu Met Lys Arg Lys Ser Ala Ser Leu Ser			
260	265	270	
val val Ala Phe Arg Val Ser Lys Ile Glu Ala Leu Gln Asn Ala Ala			
275	280	285	
val val His Ser Arg Ala Glu Asp Asn Ile Tyr Ile Val Glu Asp Arg			
290	295	300	
Pro			
305			

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<211> 918
<212> DNA
<213> Mus musculus

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tacatactta tgaaaaggaa gtcagcatct ctaagcgtgg ttgccttccg tgtctctaag 840
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gttgaagata gacccttga 918

<210> 3
<211> 282
<212> PRT
<213> Mus musculus

<220>
<221> VARIANT
<222> (1)...(282)
<223> TIM-1, C.D2 ES-HBA and DBA/2J allele

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Gly Ala Val Asp Ser Tyr Val Glu Val Lys Gly Val Val Gly His Pro
20 25 30
Val Thr Leu Pro Cys Thr Tyr Ser Thr Tyr Arg Gly Ile Thr Thr Thr
35 40 45
Cys Trp Gly Arg Gly Gln Cys Pro Ser Ser Ala Cys Gln Asn Thr Leu
50 55 60
Ile Trp Thr Asn Gly His Arg Val Thr Tyr Gln Lys Ser Ser Arg Tyr
65 70 75 80
Asn Leu Lys Gly His Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu
85 90 95
Asn Ser Val Glu Ser Asp Ser Gly Leu Tyr Cys Cys Arg Val Glu Ile
100 105 110
Pro Gly Trp Phe Asn Asp Gln Lys Val Thr Phe Ser Leu Gln Val Lys
115 120 125

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Pro Glu Ile Pro Thr Arg Pro Pro Arg Arg Pro Thr Thr Thr Arg Pro
130 135 140
Thr Ala Thr Gly Arg Pro Thr Thr Ile Ser Thr Arg Ser Thr His Val
145 150 155 160
Pro Thr Ser Thr Arg Val Ser Thr Ser Thr Pro Pro Thr Ser Thr His
165 170 175
Thr Trp Thr His Lys Pro Asp Trp Asn Gly Thr Val Thr Ser Ser Gly
180 185 190
Asp Thr Trp Ser Asn His Thr Glu Ala Ile Pro Pro Gly Lys Pro Gln
195 200 205
Lys Asn Pro Thr Lys Gly Phe Tyr Val Gly Ile Cys Ile Ala Ala Leu
210 215 220
Leu Leu Leu Leu Val Ser Thr Val Ala Ile Thr Arg Tyr Ile Leu
225 230 235 240
Met Lys Arg Lys Ser Ala Ser Leu Ser Val Val Ala Phe Arg Val Ser
245 250 255
Lys Ile Glu Ala Leu Gln Asn Ala Ala Val Val His Ser Arg Ala Glu
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Asp Asn Ile Tyr Ile Val Glu Asp Arg Pro
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<210> 4

<211> 849

<212> DNA

<213> Mus musculus

<400> 4

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gcaatcccctc caggaaagcc gcagaaaaac cctactaagg gcttctatgt tggcatctgc 660
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atgaaaagga agtcagcattc tctaagcgtg gttgccttcc gtgtctctaa gattgaagct 780
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<210> 5

<211> 305

<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> (1)...(305)

<223> TIM-2 BALB/c allele

<400> 5

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20 25 30
Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
35 40 45
Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
50 55 60

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Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile
85 90 95
Glu Asn Thr Val Val Gly Asp Gly Gly Pro Tyr Cys Cys Val Val Glu
100 105 110
Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro
115 120 125
Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro
130 135 140
Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val
145 150 155 160
Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro
165 170 175
Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu
180 185 190
Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser
195 200 205
Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro
210 215 220
Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala
225 230 235 240
Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val
245 250 255
Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile
260 265 270
Ser Lys Ile Gly Ala Ser Pro Lys Lys Val Val Glu Arg Thr Arg Cys
275 280 285
Glu Asp Gln Val Tyr Ile Ile Glu Asp Thr Pro Tyr Pro Glu Glu Glu
290 295 300
Ser
305

<210> 6
<211> 958
<212> DNA
<213> Mus musculus

<400> 6
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tcaccctgtc acacttccat gtatttattc gacacaccc tggaaatcg ttccatgtg 180
ttggggccta gggaaatgcc gccattctta ttgtatacgg tcacttatct ggaccaatgg 240
atatacggtc acacatcaga ggaacagtgc ataccagct aaggggaaata tttcagaagg 300
aaatgtgtcc ttgaccatag agaacactgt tgggggtgat ggtggccctt attgctgtgt 360
agtggagata cttggagcgt tccattttgt ggactatag ttggaaagtta aaccagaat 420
ttccacgagt ccaccaacaa ggcccacagc tacaggaaga cccacaacta tttcaacaag 480
atcccacat gtaccaacat caaccagagt ctctacctt acttctccaa caccagcaca 540
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gacagaaaat ttaccctcta ctccctgaga ctggcataac actgtgacat cctcagatga 660
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<210> 7
<211> 305
<212> PRT
<213> Mus musculus

<220>

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<221> VARIANT
<222> (1)...(305)

<223> TIM-2, C.D2 ES-HBA and DBA/2J allele

<400> 7

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20 25 30
Val Thr Leu Pro Cys Ile Tyr Ser Thr His Leu Gly Gly Ile Val Pro
35 40 45
Met Cys Trp Gly Leu Gly Glu Cys Arg His Ser Tyr Cys Ile Arg Ser
50 55 60
Leu Ile Trp Thr Asn Gly Tyr Thr Val Thr His Gln Arg Asn Ser Arg
65 70 75 80
Tyr Gln Leu Lys Gly Asn Ile Ser Glu Gly Asn Val Ser Leu Thr Ile
85 90 95
Glu Asn Thr Val Val Gly Asp Gly Pro Tyr Cys Cys Val Val Glu
100 105 110
Ile Pro Gly Ala Phe His Phe Val Asp Tyr Met Leu Glu Val Lys Pro
115 120 125
Glu Ile Ser Thr Ser Pro Pro Thr Arg Pro Thr Ala Thr Gly Arg Pro
130 135 140
Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro Thr Ser Thr Arg Val
145 150 155 160
Ser Thr Ser Thr Ser Pro Thr Pro Ala His Thr Glu Thr Tyr Lys Pro
165 170 175
Glu Ala Thr Thr Phe Tyr Pro Asp Gln Thr Thr Ala Glu Val Thr Glu
180 185 190
Thr Leu Pro Ser Thr Pro Ala Asp Trp His Asn Thr Val Thr Ser Ser
195 200 205
Asp Asp Pro Trp Asp Asp Asn Thr Glu Val Ile Pro Pro Gln Lys Pro
210 215 220
Gln Lys Asn Leu Asn Lys Gly Phe Tyr Val Gly Ile Ser Ile Ala Ala
225 230 235 240
Leu Leu Ile Leu Met Leu Leu Ser Thr Met Val Ile Thr Arg Tyr Val
245 250 255
Val Met Lys Arg Lys Ser Glu Ser Leu Ser Phe Val Ala Phe Pro Ile
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275 280 285
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290 295 300
Ser
305

<210> 8

<211> 958

<212> DNA

<213> Mus musculus

<400> 8

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tcaccctgtc acacttccat gtatttattc gacacacctt ggtggaatcg ttccttatgtg 180
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agtggagata cctggagcgt tccatttgt ggactatatg ttggaagttt aaccagaaat 420
ttccacgagt ccaccaacaa ggcccacagc tacaggaaga cccacaacta tttcaacaag 480
atccacacat gtaccaacat caaccagagt ctctacacctt acttctccaa caccagcaca 540
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ggttatcacc aggtacgtgg ttatgaaaag gaagtcaagaa tctctgagct tcgttgcctt 840
ccctatctct aagattggag cttcccccaa aaaagtggtc gaacggacca gatgtgaaga 900
ccaggtctac attattgaag acactcctta ccccgaaagaa gagtcctagt gcctctac 958

<210> 9
<211> 281
<212> PRT
<213> Mus musculus

<220>
<221> VARIANT
<222> (1)...(281)
<223> TIM-3 BALB/c allele

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20 25 30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Pro Thr Ser Gly Thr Leu
35 40 45
Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
50 55 60
Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
65 70 75 80
Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
85 90 95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
100 105 110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
115 120 125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
130 135 140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
145 150 155 160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
165 170 175
Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
180 185 190
Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu
195 200 205
Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys
210 215 220
Leu Ser Ser Leu Ser Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly
225 230 235 240
Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr
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Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr
260 265 270
Cys Tyr Val Asn Ser Gln Gln Pro Ser
275 280

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<212> DNA
<213> Mus musculus

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ccttggtcac	agtgtaccaa	tgagttgctc	agaactgatg	aaagaaaatgt	gacatatca	300
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<210> 11
<211> 281
<212> PRT
<213> Mus musculus

<220>
<221> VARIANT
<222> (1)...(281)
<223> TIM-3, C.D2 ES-HBA and DBA/2J allele

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Leu Leu Ala Arg Ser Leu Glu Asn Ala Tyr Val Phe Glu Val Gly Lys
      20          25          30
Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Ser Thr Pro Gly Ala Leu
      35          40          45

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85 90 95
Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
100 105 110
Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
115 120 125
Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
130 135 140
Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
145 150 155 160
Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
165 170 175
Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
180 185 190
Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu
195 200 205
Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys Lys
210 215 220
Leu Ser Ser Leu Ser Leu Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly
225 230 235 240
Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr
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Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr
260 265 270
Cys Tyr Val Asn Ser Gln Gln Pro Ser
275 280

<210> 12
<211> 862
<212> DNA
<213> Mus musculus

<400> 12
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caactccagct cagactgccc atggggactc tactacagct tctccaagaa ccctaaccac 480
ggagagaaat ggttcagaga cacagacact ggtgaccctc cataataaca atggaacaaa 540
aatttccaca tgggctgatg aaattaagga ctctggagaa acgatcagaa ctgctatcca 600
cattggagtg ggagtctctg ctgggttgac cctggcactt atcattggtg tcttaatct 660
taaatggtat tcctgtttaaaa aaaaaggtt atcgagttt agccttattt cactggccaa 720
cttgccctcca ggagggttgg caaatgcagg agcagtctgg attcgctctg aggaaaatat 780
ctacaccatc gaggagaacg tatatgaagt ggagaattca aatgagtaact actgctacgt 840
caacagccag cagccatcct ga 862

<210> 13
<211> 345
<212> PRT
<213> Mus musculus

<220>
<221> VARIANT
<222> (1)...(345)
<223> TIM-4, BALB/c allele

Seqlist_12_20_06.txt

<400> 13
Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Thr Glu Leu Trp Trp
1 5 10 15
Leu Tyr Leu Ser Lys Ser Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly
20 25 30
Phe Leu Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser
35 40 45
Gln Ser Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser
50 55 60
Lys Cys Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser
65 70 75 80
Arg Lys Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu
85 90 95
Val Ser Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr
100 105 110
Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn
115 120 125
Val Arg Leu Glu Leu Arg Arg Ala Thr Thr Lys Lys Pro Thr Thr
130 135 140
Thr Thr Arg Pro Thr Thr Pro Tyr Val Thr Thr Thr Pro Glu
145 150 155 160
Leu Leu Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr
165 170 175
Pro Pro Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr
180 185 190
Cys Pro Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly
195 200 205
Ser Ala Ile Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser
210 215 220
Gln Arg Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro
225 230 235 240
Thr Gly Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr
245 250 255
Gln Lys Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys
260 265 270
Ser His Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ala Cys Cys
275 280 285
Val Gly Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Leu Arg
290 295 300
Gly Lys Val Thr Gly Ala Asn Cys Leu Gln Arg His Lys Arg Pro Asp
305 310 315 320
Asn Thr Glu Val Ser Asp Ser Phe Leu Asn Asp Ile Ser His Gly Arg
325 330 335
Asp Asp Glu Asp Gly Ile Phe Thr Leu
340 345

<210> 14
<211> 1032
<212> DNA
<213> Mus musculus

<400> 14
atgtccaagg ggcttctcct cctctggctg gtgacggagc tctggtggt ttatctgaca 60
ccagctgcct cagaggatac aataataggg tttttggccc agccgggtgac tttgccttgt 120
cattacctct cgtggtcccc gagccgcaac agtatgtgt ggggcaaagg ttcatgtccc 180
aattccaagt gcaatgcaga gcttctccgt acagatggaa caagaatcat ctccaggaag 240
tcaacaaaat atacactttt ggggaagggtc cagttgggtg aagtgtccctt gaccatctca 300
aacaccaatc gaggtgacag tggggtgtac tgctgccgtt tagaggtgcc tggctgggttc 360
aatgatgtca agaagaatgt gcgctggag ctgaggagag ccacaacaac caaaaaacca 420
acaacaacca cccggccaac caccacccct tatgttaacca ccaccacccc agagctgctt 480
ccaacaacag tcatgaccac atctgttctt ccaaccacca caccacccca gacactagcc 540

Seqlist_12_20_06.txt

accactgcct tcagtagc agtgaccacg tgcccccaa caacacctgg ctcccttctca 600
caagaaacca caaaaagggtc cgccatcaact acagaatcag aaactctgcc tgcataatccat 660
caactctaaa gaagcatgat gaccatatct acagacatag ccgtactcg gcccacaggc 720
tctaaccctg ggattctccc atccacttca cagctgacga cacagaaaac aacattaaca 780
acaagtgagt ctttgagaa gacaactaaa tcacatcaga tcaacacgac acagaccatc 840
ttgatcattg cctgctgtgt gggatttgtt ctaatgggtt tattgtttctt ggcgtttctc 900
cttcgagggaa aagtccacagg agccaactgt ttgcagagac acaagaggcc agacaacact 960
gaagatagtg acagcgtcct caatgacatg tcacacggga gggatgatga agacgggatc 1020
ttcactctct ga 1032

<210> 15
<211> 345
<212> PRT
<213> Mus musculus

<220>
<221> VARIANT
<222> (1)...(345)
<223> C.D2 ES-HBA and DBA/2J allele

<400> 15
Met Ser Lys Gly Leu Leu Leu Leu Trp Leu Val Met Glu Leu Trp Trp
1 5 10 15
Leu Tyr Leu Ser Lys Ser Pro Ala Ala Ser Glu Asp Thr Ile Ile Gly
20 25 30
Phe Leu Gly Gln Pro Val Thr Leu Pro Cys His Tyr Leu Ser Trp Ser
35 40 45
Gln Ser Arg Asn Ser Met Cys Trp Gly Lys Gly Ser Cys Pro Asn Ser
50 55 60
Lys Cys Asn Ala Glu Leu Leu Arg Thr Asp Gly Thr Arg Ile Ile Ser
65 70 75 80
Arg Lys Ser Thr Lys Tyr Thr Leu Leu Gly Lys Val Gln Phe Gly Glu
85 90 95
Val Ser Leu Thr Ile Ser Asn Thr Asn Arg Gly Asp Ser Gly Val Tyr
100 105 110
Cys Cys Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Lys Asn
115 120 125
Val Arg Leu Glu Leu Arg Arg Ala Thr Thr Thr Lys Lys Pro Thr Thr
130 135 140
Thr Thr Arg Pro Thr Thr Pro Tyr Val Thr Thr Thr Thr Pro Glu
145 150 155 160
Leu Leu Pro Thr Thr Val Met Thr Thr Ser Val Leu Pro Thr Thr
165 170 175
Pro Pro Gln Thr Leu Ala Thr Thr Ala Phe Ser Thr Ala Val Thr Thr
180 185 190
Cys Pro Ser Thr Thr Pro Gly Ser Phe Ser Gln Glu Thr Thr Lys Gly
195 200 205
Ser Ala Phe Thr Thr Glu Ser Glu Thr Leu Pro Ala Ser Asn His Ser
210 215 220
Gln Arg Ser Met Met Thr Ile Ser Thr Asp Ile Ala Val Leu Arg Pro
225 230 235 240
Thr Gly Ser Asn Pro Gly Ile Leu Pro Ser Thr Ser Gln Leu Thr Thr
245 250 255
Gln Lys Thr Thr Leu Thr Thr Ser Glu Ser Leu Gln Lys Thr Thr Lys
260 265 270
Ser His Gln Ile Asn Ser Arg Gln Thr Ile Leu Ile Ile Ala Cys Cys
275 280 285
Val Gly Phe Val Leu Met Val Leu Leu Phe Leu Ala Phe Leu Leu Arg
290 295 300
Gly Lys Val Thr Gly Ala Asn Cys Leu Gln Arg His Lys Arg Pro Asp
305 310 315 320
Asn Thr Glu Val Ser Asp Ser Phe Leu Asn Asp Ile Ser His Gly Arg
325 330 335

Seqlist_12_20_06.txt

Asp Asp Glu Asp Gly Ile Phe Thr Leu
340 345

<210> 16
<211> 1032
<212> DNA
<213> Mus musculus

<400> 16
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ccagctgcct cagaggatac aataataggg tttttgggcc agccggtgac tttgccttgt 120
cattacctct cgtggtccca gagccgcaac agtatgtgt ggggcaaagg ttcatgtccc 180
aattccaagt gcaatgcaga gcttcctcgat acagatggaa caagaatcat ctccaggaag 240
tcaacaaaat atacactttt ggggaagggtc cagtttgggtg aagtgtcctt gaccatctca 300
aacaccaatc gaggtgacag tgggggtgtac tgctgcccgtataggggtcc tggctggttc 360
aatgtatgtca agaagaatgt ggcgttggag ctgaggagag ccacaacaac caaaaaaacca 420
acaacaacca cccggccaac caccacccct tatgtAACCA ccaccacccc agagctgctt 480
ccaacaacag tcatgaccac atctgttctt ccaaccacca caccacccca gacactagcc 540
accactgcct tcagtagcgc agtggaccacg tgccccctcaa caacacctgg ctccttctca 600
caagaaacca caaaaagggtc cgccttact acagaatcag aaactctgcc tgcacatccaat 660
caactctaaa gaagcatgat gaccatatct acagacatag ccgtactcag gcccacaggc 720
tctaaccctg ggattctccc atccacttca cagctgacga cacagaaaac aacattaaca 780
acaagtgagt ctttgcagaa gacaactaaa tcacatcaga tcaacagcag acagaccatc 840
ttgatcatttgcctgctgtgt gggatttgggttctt ggcgtttctc 900
cttcgaggga aagtccacagg agccaaactgt ttgcagagac acaagaggcc agacaacact 960
gaagatagtg acagcgtcct caatgacatg tcacacggga gggatgatga agacgggatc 1020
ttcactctctt ga 1032

<210> 17
<211> 359
<212> PRT
<213> H. sapiens

<220>
<221> VARIANT
<222> (1)...(360)
<223> TIM-1 allele 1

<400> 17
Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
1 5 10 15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
20 25 30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
35 40 45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
50 55 60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
65 70 75 80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
85 90 95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100 105 110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
115 120 125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130 135 140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Val Pro Thr Thr Thr
145 150 155 160
Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Val Pro Thr Thr
165 170 175
Met Thr Val Ser Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro

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180	185	190
Thr Thr Thr Ser Val Pro Val Thr Thr Thr Val Ser Thr Phe Val Pro		
195	200	205
Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro		
210	215	220
Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Ala		
225	230	235
Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp		
245	250	255
Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Asn Asn Asn		
260	265	270
Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr		
275	280	285
Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala		
290	295	300
Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val		
305	310	315
Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln		
325	330	335
Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu		
340	345	350
Asn Ser Leu Tyr Ala Thr Asp		
355		

<210> 18
<211> 1080
<212> DNA
<213> H. sapiens

<400> 18
atgcatcctc aagtggcat cttaagcctc atcctacatc tggcagattc ttagctgg 60
tctgttaagg ttggggaga ggcaggcca tctgtcacac taccctgca ctacagtgg 120
gctgtcacat caatgtctg gaatagaggc tcattttctc tattcacatg caaaaatggc 180
attgtctgga ccaatggAAC ccacgtcacc tatcgaaagg acacacgcta taagctattg 240
ggggacctt caagaaggga tgtctttt accatagaaa atacagctgt gtctgacagt 300
ggcgtatatt gttgccgtg tgacaccgt ggggtggcca atgacatgaa aatcaccgt 360
tcattggaga ttgtgccacc caaggtcacc actactccaa ttgtcacaac tgttccaacc 420
gtcacactg ttcaacacg caccactgtt ccaacgcaca cgactgttcc aacgacaact 480
gttccaaaca caatgagcat tccaaacgaca acgactgttcc cgacgacaat gactgtttca 540
acgacaacga gcgttccaac gacaacgagc attccaacaa caacaagtgt tccagtgaca 600
acaacggctt ctacctttgt tcctccaatg ctttgccccca ggcagaacca tgaaccagta 660
gccacttcac catcttcacc tcagccagca gaaacccacc ctacgacact gcagggagca 720
ataaggagag aaccccaccag ctcaccattt tactcttaca caacagatgg gaatgacacc 780
gtgacagagt cttcagatgg ctttggaa aacaatcaa ctcactgtt cctagaacat 840
agtctactga cggccaatac cactaaagga atctatgctg gagtctgtat ttctgtctg 900
gtgcttcttg ctcttttggg tgtcatcatt gccaaaaagt atttcttcaa aaaggaggtt 960
caacaactaa gtgtttcatt tagcagcctt caaattaaag ctttgcaaaa tgcagttgaa 1020
aaggaagtcc aagcagaaga caatatctac attgagaata gtcttatgc cacggactaa 1080

<210> 19
<211> 359
<212> PRT
<213> H. sapiens

<220>
<221> VARIANT
<222> (1)...(359)
<223> TIM-1, allele 2

<400> 19
Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp

seqlist_12_20_06.txt

1	5	10	15													
Ser	Val	Ala	Gly	Ser	Val	Lys	Val	Gly	Gly	Glu	Ala	Gly	Pro	Ser	Val	
							20	25							30	
Thr	Leu	Pro	Cys	His	Tyr	Ser	Gly	Ala	Val	Thr	Ser	Met	Cys	Trp	Asn	
												35		45		
Arg	Gly	Ser	Cys	Ser	Leu	Phe	Thr	Cys	Gln	Asn	Gly	Ile	Val	Trp	Thr	
												50	55	60		
Asn	Gly	Thr	His	Val	Thr	Tyr	Arg	Lys	Asp	Thr	Arg	Tyr	Lys	Leu	Leu	
												65	70	75	80	
Gly	Asp	Leu	Ser	Arg	Arg	Asp	Val	Ser	Leu	Thr	Ile	Glu	Asn	Thr	Ala	
												85	90	95		
Val	Ser	Asp	Ser	Gly	Val	Tyr	Cys	Cys	Arg	Val	Glu	His	Arg	Gly	Trp	
												100	105	110		
Phe	Asn	Asp	Asp	Met	Lys	Ile	Thr	val	Ser	Leu	Glu	Ile	Val	Pro	Pro	Lys
												115	120	125		
Val	Thr	Thr	Thr	Pro	Ile	Val	Thr	Thr	Val	Pro	Thr	Val	Thr	Thr	Val	
												130	135	140		
Arg	Thr	Ser	Thr	Thr	Val	Pro	Thr	Thr	Thr	Val	Pro	Thr	Thr	Thr		
												145	150	155	160	
Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr	Thr	Val	Pro	Thr	Thr		
												165	170	175		
Met	Thr	Val	Ser	Thr	Thr	Ser	Val	Pro	Thr	Thr	Thr	Ser	Ile	Pro		
												180	185	190		
Thr	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Ala	Val	Ser	Thr	Phe	Val	Pro	
												195	200	205		
Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu	Pro	Val	Ala	Thr	Ser	Pro	
												210	215	220		
Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro	Thr	Thr	Leu	Gln	Gly	Ala	
												225	230	235	240	
Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu	Tyr	Ser	Tyr	Thr	Asp		
												245	250	255		
Gly	Asn	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp	Gly	Leu	Trp	Asn	Asn	Asn	
												260	265	270		
Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu	Leu	Thr	Ala	Asn	Thr	Thr	
												275	280	285		
Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser	Val	Leu	Val	Leu	Leu	Ala	
												290	295	300		
Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr	Phe	Phe	Lys	Lys	Glu	Val	
												305	310	315	320	
Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu	Gln	Ile	Lys	Ala	Leu	Gln	
												325	330	335		
Asn	Ala	Val	Glu	Lys	Glu	Val	Gln	Ala	Glu	Asp	Asn	Ile	Tyr	Ile	Glu	
												340	345	350		
Asn	Ser	Leu	Tyr	Ala	Thr	Asp						355				

<210> 20
<211> 1080
<212> DNA
<213> H. sapiens

<400> 20
atgcatccctc aagtggcat cttaaagcctc atcctacatc tggcagattc tgttagcttgt 60
tctgttaaagg ttgggtggaga ggcaggatcca tctgtcacac taccctgcca ctacagtggaa 120
gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg caaaaatggc 180
attgtctggaa ccaatggaaac ccacgtcacc tatcggaagg acacacgcta taagctattg 240
ggggaccttt caagaaggaa tgcgtctttt accatagaaa atacagctgt gtctgacagt 300
ggcgttatatt gttgccgtgt tgagcaccgt gggtggttca atgacatgaa aatcaccgtt 360
tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tgttccaacc 420
gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aacgacaact 480
gttccaaacaa caatgagcat tccaaacgaca acgactgttc cgacgacaat gactgtttca 540
acgacaacga gcgttccaac gacaacgagc attccaaacaa caacaagtgt tccagtgaca 600

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acagcggtct ctaccttgc tcctccaatg cctttggccca ggcagaacca tgaaccagta 660
gccacttcac catttcacc tcagccagca gaaacccacc ctacgacact gcagggagca 720
ataaggagag aacccaccag ctcaccattg tactcttaca caacagatgg gaatgacacc 780
gtgacagagt cttcagatgg cctttgaat aacaatcaa ctcaactgtt cctagaacat 840
agtctactga cggccaatac cactaaagga atctatgctg gagtctgtat ttctgtctg 900
gtgcttcttg ctctttggg tgtcatcatt gccaaaaagt atttcttcaa aaaggaggtt 960
caacaactaa gtgtttcatt tagcagcctt caaattaaag ctttgcaaaa tgcagttgaa 1020
aaggaagtcc aagcagaaga caatatctac attgagaata gtctttatgc cacggactaa 1080

<210> 21
<211> 365
<212> PRT
<213> H. sapiens

<220>
<221> VARIANT
<222> (1)...(365)
<223> TIM-1, allele 3

<400> 21
Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
1 5 10 15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
20 25 30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
35 40 45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
50 55 60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
65 70 75 80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
85 90 95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100 105 110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
115 120 125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130 135 140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Thr Val Pro Met Thr Thr
145 150 155 160
Thr Val Pro Thr Thr Val Pro Thr Thr Met Ser Ile Pro Thr Thr
165 170 175
Thr Thr Val Pro Thr Thr Met Thr Val Ser Thr Thr Ser Val Pro
180 185 190
Thr Thr Thr Ser Ile Pro Thr Thr Ser Val Pro Val Thr Thr Ala
195 200 205
Val Ser Thr Phe Val Pro Pro Met Pro Leu Pro Arg Gln Asn His Glu
210 215 220
Pro Val Ala Thr Ser Pro Ser Ser Pro Gln Pro Ala Glu Thr His Pro
225 230 235 240
Thr Thr Leu Gln Gly Ala Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu
245 250 255
Tyr Ser Tyr Thr Asp Gly Asn Asp Thr Val Thr Glu Ser Ser Asp
260 265 270
Gly Leu Trp Asn Asn Asn Gln Thr Gln Leu Phe Leu Glu His Ser Leu
275 280 285
Leu Thr Ala Asn Thr Thr Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser
290 295 300
Val Leu Val Leu Leu Ala Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr
305 310 315 320
Phe Phe Lys Lys Glu Val Gln Gln Leu Ser Val Ser Phe Ser Ser Leu
325 330 335

Seqlist_12_20_06.txt

Gln Ile Lys Ala Leu Gln Asn Ala Val Glu Lys Glu Val Gln Ala Glu
340 345 350
Asp Asn Ile Tyr Ile Glu Asn Ser Leu Tyr Ala Thr Asp
355 360 365

<210> 22
<211> 1098

<212> DNA

<213> H. sapiens

<400> 22

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gctgtcacat caatgtgctg gaataggc tcatgttctc tattcacatg caaaaatg 180
attgtctgga ccaatggaa ccacgtcacc tatcggagg acacacgcta taagctattg 240
ggggacctt caagaaggga tgtctttt accatagaaa atacagctgt gtctgacagt 300
ggcgatatt gttgccgtg tgagcaccgt ggggtggfca atgacatgaa aatcaccgt 360
tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac ttttccaacc 420
gtcacactg ttcaacccgag caccactgtt ccaacgacaa cgactgttcc aatgacaacg 480
actgtccaa cgacaactgt tccacaaca atgagcattc caacgacaac gactgttccg 540
acgacaatga ctgtttcaac gacaacgagc gttccaacga caacgagcat tccaacaaca 600
acaagtgttc cagtgacaac arcggctct acctttgttc ctccaatgcc tttgcccagg 660
cagaaccatg aaccagtgc cacttcacca tttcaccc agccagcaga aacccaccct 720
acgacactgc agggagcaat aaggagagaa cccaccagct caccattgtt ctcttacaca 780
acagatggga atgacaccgt gacagagtct tcagatggcc tttgaataa caatcaaact 840
caactgtcc tagaacatag tctactgacg gccaataccca ctaaaggaat ctatgctgga 900
gtctgtattt ctgtcttggg gcttcttgct ctttgggtg tcatttttttgc caaaaagtat 960
ttcttcaaaa aggaggttca acaactaagt gtttcatat gcagccttca aattaaagct 1020
ttgcaaaaatg cagttgaaaaa ggaagtccaa gcagaagaca atatctacat tgagaatagt 1080
ctttatgcca cggactaa 1098

<210> 23

<211> 359

<212> PRT

<213> H. sapiens

<220>

<221> VARIANT

<222> (1)...(359)

<223> TIM-1, allele 4

<400> 23

Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
1 5 10 15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
20 25 30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
35 40 45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
50 55 60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
65 70 75 80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
85 90 95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100 105 110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
115 120 125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130 135 140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Val Pro Thr Thr Thr
145 150 155 160

Seqlist_12_20_06.txt

Val	Pro	Thr	Thr	Met	Ser	Ile	Pro	Thr	Thr	Thr	Thr	Val	Pro	Thr	Thr
165								170					175		
Met	Thr	Val	Ser	Thr	Thr	Thr	Ser	Val	Pro	Thr	Thr	Thr	Ser	Ile	Pro
180								185					190		
Thr	Thr	Thr	Ser	Val	Pro	Val	Thr	Thr	Ser	Val	Ser	Thr	Phe	Val	Pro
195							200					205			
Pro	Met	Pro	Leu	Pro	Arg	Gln	Asn	His	Glu	Pro	Val	Ala	Thr	Ser	Pro
210						215			220						
Ser	Ser	Pro	Gln	Pro	Ala	Glu	Thr	His	Pro	Thr	Thr	Leu	Gln	Gly	Thr
225						230				235				240	
Ile	Arg	Arg	Glu	Pro	Thr	Ser	Ser	Pro	Leu	Tyr	Ser	Tyr	Thr	Asp	
245								250					255		
Gly	Asn	Asp	Thr	Val	Thr	Glu	Ser	Ser	Asp	Gly	Leu	Trp	Ser	Asn	Asn
260							265					270			
Gln	Thr	Gln	Leu	Phe	Leu	Glu	His	Ser	Leu	Leu	Thr	Ala	Asn	Thr	Thr
275						280					285				
Lys	Gly	Ile	Tyr	Ala	Gly	Val	Cys	Ile	Ser	Val	Leu	Val	Leu	Leu	Ala
290						295					300				
Leu	Leu	Gly	Val	Ile	Ile	Ala	Lys	Lys	Tyr	Phe	Phe	Lys	Lys	Glu	Val
305						310				315				320	
Gln	Gln	Leu	Ser	Val	Ser	Phe	Ser	Ser	Leu	Gln	Ile	Lys	Ala	Leu	Gln
325									330				335		
Asn	Ala	Val	Glu	Lys	Glu	Val	Gln	Ala	Glu	Asp	Asn	Ile	Tyr	Ile	Glu
340									345				350		
Asn	Ser	Leu	Tyr	Ala	Thr	Asp									
															355

<210> 24
<211> 1079
<212> DNA
<213> H. sapiens

<400> 24
atgcatccctc aagtggcat cttaaggcctc atcctacatc tggcagattc ttagctgg 60
tctgtaaagg ttggggaga ggcagggtcca tctgtcacac taccctgcca ctacagtgg 120
gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg caaaaatggc 180
attgtctgga ccaatggAAC ccacgtcacc tatacgaaagg acacacgcta taagctattg 240
ggggaccttt caagaaggaga tgtcttttg accatagaaa atacagctgt gtctgacagt 300
ggcgatattt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa ataccggta 360
tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tggttccaacc 420
gtcaccactg ttcaaacggag caccactgtt ccaacgacaa cgactgttcc aacgacaact 480
gttccaaaca caatgagcat tccaaacgaca acggactgtt ccgacgacaa tgactgtt 540
aacgacaacg agcgttccaa cgacaaacgag cattccaaaca acaacaagtg ttccagtgac 600
aacatgtctc tactttgtt cctccaaatgc ctttggccag gcagaaccat gaaccagttag 660
ccacttcacc atcttcacct cagccagcag aaacccaccc tacgacactg cagggagcaa 720
taaggagaga acccaccaggc tcaccattgt actcttacac aacagatggg aatgacaccc 780
tgacagagtc ttccatgtggc ctttggarta acaatcaaac tcaactgttcc ctggaaacata 840
gtctactgac ggccaataacc actaaaggaa tctatgttgg agtctgtatt tctgtcttgg 900
tgctttctgc tctttgggt gtcatcattt caaaaaaatgtt tttcttcaaa aaggagggttc 960
aacaactaag ttgttccattt agcaggccttc aaattaaagc ttggaaaat gcagttgaaa 1020
aggaaagtccaa agcagaagac aatatctaca ttggaaatag tctttatgccc acggactaa 1079

<210> 25
<211> 364
<212> PRT
<213> H. sapiens

<220>
<221> VARIANT
<222> (1)...(364)
<223> TIM-1 allele 5

seqlist_12_20_06.txt

<400> 25
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1 5 10 15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
20 25 30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
35 40 45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
50 55 60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
65 70 75 80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
85 90 95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100 105 110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
115 120 125
Val Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130 135 140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Val Pro Met Thr Thr
145 150 155 160
Thr Val Pro Thr Thr Val Pro Thr Thr Met Ser Ile Pro Thr Thr
165 170 175
Thr Thr Val Pro Thr Thr Met Thr Val Ser Thr Thr Thr Ser Val Pro
180 185 190
Thr Thr Thr Ser Ile Pro Thr Thr Ser Val Pro Val Thr Thr Thr Val
195 200 205
Ser Thr Phe Val Pro Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro
210 215 220
Val Ala Thr Ser Pro Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr
225 230 235 240
Thr Leu Gln Gly Ala Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr
245 250 255
Ser Tyr Thr Asp Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly
260 265 270
Leu Trp Asn Asn Asn Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu
275 280 285
Thr Ala Asn Thr Thr Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val
290 295 300
Leu Val Leu Leu Ala Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe
305 310 315 320
Phe Lys Lys Glu Val Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln
325 330 335
Ile Lys Ala Leu Gln Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp
340 345 350
Asn Ile Tyr Ile Glu Asn Ser Leu Tyr Ala Thr Asp
355 360

<210> 26
<211> 1095
<212> DNA
<213> H. sapiens

<400> 26
atgcatccctc aagtggcat cttaaggc ctc atcctacatc tggcagattc ttagctgg 60
tctgtaaagg ttggggaga ggcagg tcca tctgtcac ac taccctgcca ctacagt gga 120
gctgtcacat caatgtgctg gaatagaggc tcatgttctc tattcacatg caaaaatggc 180
attgtctgga ccaatggAAC ccacgtcacc tatcgaaagg acacacgcta taagctattg 240
ggggaccttt caagaaggga tgtctttt accatagaaa atacagctgt gtctgacagt 300
ggcgatatt gttgccgtgt tgagcaccgt gggtggatca atgacatgaa aatcaccgt 360
tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tggtccaacc 420
gtcacgactg ttcgaacgag caccactgtt ccaacgacaa cgactgttcc aatgacaacg 480

Seqlist_12_20_06.txt

actgttccaa cgacaactgt tccaacaaca atgagcattc caacgacaac gactgttccg 540
acgacaatga ctgtttcaac gacaacgagc gttccaacga caacgagcat tccaacaaca 600
agtgttccag tgacaacaac ggtcttacc tttgttcctc caatgcctt gcccaggcag 660
aaccatgaac cagtagccac ttccacatct tcacctcagc cagcagaaac ccaccctacg 720
acactgcagg gagcaataag gagagaaccc accagctcac cattgtactc ttacacaaca 780
gatgggaatg acaccgtac agagttca gatggcctt ggaataacaa tcaaactcaa 840
ctgttccctag aacatagtct actgacggcc aataccacta aaggaatcta tgctggagtc 900
tgtatTTCTG tcttggtgtc tcttgctt ttgggtgtca tcattgccaa aaagtatttc 960
ttcaaaaagg aggttcaaca actaagtgtt tcatttagca gccttcaa at taaagctt 1020
caaaatgcag ttgaaaagga agtccaagca gaagacaata tctacattga gaatagtctt 1080
tatgccacgg actaa 1095

<210> 27
<211> 364
<212> PRT
<213> H. sapiens

<220>
<221> VARIANT
<222> (1)...(364)
<223> TIM-1, allele 6

<400> 27
Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
1 5 10 15
Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
20 25 30
Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
35 40 45
Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
50 55 60
Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
65 70 75 80
Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
85 90 95
Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
100 105 110
Phe Asn Asp Met Lys Ile Thr Val Ser Leu Gly Ile Val Pro Pro Lys
115 120 125
Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
130 135 140
Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Val Pro Met Thr Thr
145 150 155 160
Thr Val Pro Thr Thr Val Pro Thr Thr Met Ser Ile Pro Thr Thr
165 170 175
Thr Thr Val Pro Thr Thr Met Thr Val Ser Thr Thr Thr Ser Val Pro
180 185 190
Thr Thr Thr Ser Ile Pro Thr Thr Ser Val Pro Val Thr Thr Thr Val
195 200 205
Ser Thr Phe Val Pro Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro
210 215 220
Val Ala Thr Ser Pro Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr
225 230 235 240
Thr Leu Gln Gly Ala Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr
245 250 255
Ser Tyr Thr Thr Asp Gly Asp Asp Thr Val Thr Glu Ser Ser Asp Gly
260 265 270
Leu Trp Asn Asn Asn Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu
275 280 285
Thr Ala Asn Thr Thr Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val
290 295 300
Leu Val Leu Leu Ala Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe
305 310 315 320

Seqlist_12_20_06.txt

Phe Lys Lys Glu Val Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln
325 330 335
Ile Lys Ala Leu Gln Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp
340 345 350
Asn Ile Tyr Ile Glu Asn Ser Leu Tyr Ala Thr Asp
355 360

<210> 28
<211> 1099

<212> DNA

<213> H. sapiens

<400> 28

atgcatcctc aagtggcat cttaaggctc atcctacatc tggcagattc ttagctgg 60
tctgtaaagg ttggggaga ggcaggcca tctgtcacac taccctgcca ctacagtgg 120
gctgtcacat caatgtgctg gaatagaggg tcatagttctc tattcacatg caaaaatggc 180
attgtctgga ccaatggAAC ccacgtcacc tateggaaagg acacacgcta taagctattg 240
ggggaccttt caagaaggaa tgtcttttg accatagaaa atacagctgt gtctgacagt 300
ggcgatatt gttgccgtgt tgagcaccgt ggggtggttca atgacatgaa aatcaccgt 360
tcattggaga ttgtgccacc caaggtcacg actactccaa ttgtcacaac tggccaacc 420
gtcagactg ttcaacggag caccactgtt ccaacgacaa cgactgttcc aatgacaacc 480
gactgttcca acgacaactg ttccaaacaac aatgagcatt ccaacgacaa cgactgttcc 540
gacgacaatg actgtttcaa cgacaacggag cggttccaacg acaacgagca ttccaaacaac 600
aacaagtgtt ccagtgacaa caacggcttc tacctttgtt cctccaatgc ctttgcccag 660
gcagaaccat gaaccaggtag ccacttcacc atcttcaccc cagccagcag aaacccaccc 720
tacgacactg cagggagcaa taaggagaga acccaccagg tcaccattgt actcttacac 780
aacagatggg gatgacaccc tgacagagtc ttcatgtgc ctttggaaa acaatcaaac 840
tcaactgttc cttagaacata gtctactgac gccaataacc actaaaggaa tctatgctgg 900
agtctgtatt tctgtcttgg tgcttcttgc tctttgggt gtcatcattg caaaaagta 960
tttctcaaa aaggagggttc aacaactaag tttttcattt agcagccccc aaattaaagc 1020
tttgcaaaat gcagttgaaa aggaagtcca agcagaagac aatatctaca ttgagaatag 1080
tcttatgcc acggactaa 1099

<210> 29

<211> 301

<212> PRT

<213> H. sapiens

<220>

<221> VARIANT

<222> (1)...(301)

<223> TIM-3, allele 1

<400> 29

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu
1 5 10 15
Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
20 25 30
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
35 40 45
Val Pro Val Cys Trp Gly Lys Ala Cys Pro Val Phe Glu Cys Gly
50 55 60
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65 70 75 80
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
85 90 95
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
100 105 110
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
115 120 125
Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
130 135 140

Seqlist_12_20_06.txt

Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
145 150 155 160
Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
165 170 175
Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
180 185 190
Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
195 200 205
Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe
210 215 220
Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile
225 230 235 240
Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu
245 250 255
Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr
260 265 270
Glu Val Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln
275 280 285
Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
290 295 300

<210> 30
<211> 1116
<212> DNA
<213> H. sapiens

<400> 30
ggagagttaa aactgtgcct aacagaggta tcctctgact tttcttctgc aagctccatg 60
tttcacatc ttccctttga ctgtgtcctg ctgctgctgc tgctactact tacaagggtcc 120
tcagaagtgg aatacagagc ggaggtcggt cagaatgcct atctgccctg cttctacacc 180
ccagccccc cagggAACCT cgtgcccgtc tgctggggca aaggagcctg tcctgtgttt 240
aatgtggca acgtgggtgtc caggactgat gaaagggtat tgaattattt gacatccaga 300
tactggctaa atggggattt ccgcaaaaggta gatgtgtccct tgaccataga gaatgtgact 360
ctagcagaca gtggggatcta ctgctgcccgg atccaaatccc caggcataat gaatgtatgaa 420
aaatttaacc tqaagggtgtt catcaaacc gccaagggtca cccctgcacc gactctgcag 480
agagacttca ctgcagccct tccaaaggatg cttaccacca ggggacatgg cccagcagag 540
acacagacac tggggagccct ccctgatata aatctaacc ac aatatccac attggccat 600
gagttacggg actcttagatt gccaatgac ttacgggact ctggagcaac catcagaata 660
ggcatctaca tcggaggcagg gatctgtgtc gggctggctc tggcttttat cttccggcgt 720
ttaattttca aatggatttc tcatagcaaa gagaagatac agaatttaag cctcatctt 780
ttggcccaacc tccctccctc aggattggca aatgcagtag cagagggat tgcgtcagaa 840
gaaaacatct ataccattga agagaacgta tatgaagtgg aggagccaa tgagtattat 900
tgctatgtca gcagcaggca gcaaccctca caacctttgg gttgtcgctt tgcaatgcct 960
tagatccaac caccttattt ttgagcttgg tgtttgcct tttcagaaa ctatgagctg 1020
tgtcacctga ctggttttgg aggttctgtc cactgctatg gagcagagtt ttcccatttt 1080
cagaagataa tgactcacat gggaaattgaa ctggga 1116

<210> 31
<211> 301
<212> PRT
<213> H. sapiens

<220>
<221> VARIANT
<222> (1)...(301)
<223> TIM-3, allele 2

<400> 31
Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu
1 5 10 15
Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
20 25 30

Seqlist_12_20_06.txt

Asn	Ala	Tyr	Leu	Pro	Cys	Phe	Tyr	Thr	Pro	Ala	Ala	Pro	Gly	Asn	Leu
35						40						45			
Val	Pro	Val	Cys	Trp	Gly	Lys	Gly	Ala	Cys	Pro	Val	Phe	Glu	Cys	Gly
50						55					60				
Asn	Val	Val	Leu	Arg	Thr	Asp	Glu	Arg	Asp	Val	Asn	Tyr	Trp	Thr	Ser
65						70				75			80		
Arg	Tyr	Trp	Leu	Asn	Gly	Asp	Phe	Arg	Lys	Gly	Asp	Val	Ser	Leu	Thr
						85			90			95			
Ile	Glu	Asn	Val	Thr	Leu	Ala	Asp	Ser	Gly	Ile	Tyr	Cys	Cys	Arg	Ile
						100			105			110			
Gln	Ile	Pro	Gly	Ile	Met	Asn	Asp	Glu	Lys	Phe	Asn	Leu	Lys	Leu	Val
						115			120			125			
Ile	Lys	Pro	Ala	Lys	Val	Thr	Pro	Ala	Pro	Thr	Leu	Gln	Arg	Asp	Phe
						130			135			140			
Thr	Ala	Ala	Phe	Pro	Arg	Met	Leu	Thr	Thr	Arg	Gly	His	Gly	Pro	Ala
145						150				155			160		
Glu	Thr	Gln	Thr	Leu	Gly	Ser	Leu	Pro	Asp	Ile	Asn	Leu	Thr	Gln	Ile
						165			170			175			
Ser	Thr	Leu	Ala	Asn	Glu	Leu	Arg	Asp	Ser	Arg	Leu	Ala	Asn	Asp	Leu
						180			185			190			
Arg	Asp	Ser	Gly	Ala	Thr	Ile	Arg	Ile	Gly	Ile	Tyr	Ile	Gly	Ala	Gly
						195			200			205			
Ile	Cys	Ala	Gly	Leu	Ala	Leu	Ala	Leu	Ile	Phe	Gly	Ala	Leu	Ile	Phe
						210			215			220			
Lys	Trp	Tyr	Ser	His	Ser	Lys	Glu	Lys	Ile	Gln	Asn	Leu	Ser	Leu	Ile
225						230			235			240			
Ser	Leu	Ala	Asn	Leu	Pro	Pro	Ser	Gly	Leu	Ala	Asn	Ala	Val	Ala	Glu
						245			250			255			
Gly	Ile	Arg	Ser	Glu	Glu	Asn	Ile	Tyr	Thr	Ile	Glu	Glu	Asn	Val	Tyr
						260			265			270			
Glu	Val	Glu	Glu	Pro	Asn	Glu	Tyr	Tyr	Cys	Tyr	Val	Ser	Ser	Arg	Gln
						275			280			285			
Gln	Pro	Ser	Gln	Pro	Leu	Gly	Cys	Arg	Phe	Ala	Met	Pro			
						290			295			300			

<210> 32
<211> 1116
<212> DNA
<213> H. sapiens

<400> 32						
ggagagttaa	aactgtgcct	aacagaggta	tcctctgact	tttcttctgc	aagctccatg	60
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tcagaagtgg	aatacagagc	ggaggtcggt	cagaatgcct	atctgcccctg	tttcttacacc	180
ccagccgccc	cagggaacct	cgtgcccgtc	tgctggggca	aaggagcctg	tcctgtgttt	240
gaatgtggca	acgtgggtgc	caggactgat	gaaagggtatg	tgaattattg	gacatccaga	300
tactggctaa	atggggattt	ccgcaaagga	gatgtgtccc	tgaccataga	aatgtgtact	360
ctagcagaca	gtgggatcta	ctgctgccgg	atccaaatcc	caggcataat	aatgtatgaa	420
aaatttttaacc	tgaagtttgtt	catcaaacc	gccaagggtca	ccccctgcacc	gactcggcag	480
agagacttca	ctgcagccct	tccaaaggatg	cttaccacca	ggggacatgg	cccagcagag	540
acacagacac	tggggagcct	ccctgtatata	aatctaacc	aaatatccac	attggccat	600
gagttacggg	actcttagtt	ggccaaatgac	ttacgggact	ctggagcaac	catcagaata	660
ggcatactaca	tccggcagg	gatctgtgc	gggctggctc	tggcttttat	tttcggcgct	720
ttaattttca	aatggttattt	tcatagcaaa	gagaagatac	agaatttaag	cctcatct	780
ttggccaaacc	tccctccctc	aggatggca	aatgcagtag	cagaggaaat	tcgctcagaa	840
aaaaacatct	ataccattga	agagaacgta	tatgaagtgg	aggagcccaa	tgagtttat	900
tgctatgtca	gcagcaggca	gcaaccctca	caacctttgg	gttgcgcctt	tgcaatgcct	960
tagatccaaac	caccttattt	ttgagcttgg	tgttttgtct	ttttcagaaa	cstatgagctg	1020
tgtcacctga	ctggttttgg	aggttctgtc	cactgctatg	gagcagagtt	ttccccatttt	1080
cagaagataa	tgactcacat	ggaaatttggaa	ctgggaa			1116

<210> 33

Seqlist_12_20_06.txt

<211> 378
<212> PRT
<213> H. sapiens

<220>
<221> VARIANT
<222> (1)...(378)
<223> TIM-4, allele 1

<400> 33
Met Ser Lys Glu Pro Leu Ile Leu Trp Leu Met Ile Glu Phe Trp Trp
1 5 10 15
Leu Tyr Leu Thr Pro Val Thr Ser Glu Thr Val Val Thr Glu Val Leu
20 25 30
Gly His Arg Val Thr Leu Pro Cys Leu Tyr Ser Ser Trp Ser His Asn
35 40 45
Ser Asn Ser Met Cys Trp Gly Lys Asp Gln Cys Pro Tyr Ser Gly Cys
50 55 60
Lys Glu Ala Leu Ile Arg Thr Asp Gly Met Arg Val Thr Ser Arg Lys
65 70 75 80
Ser Ala Lys Tyr Arg Leu Gln Gly Thr Ile Pro Arg Gly Asp Val Ser
85 90 95
Leu Thr Ile Leu Asn Pro Ser Glu Ser Asp Ser Gly Val Tyr Cys Cys
100 105 110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Ile Asn Val Arg
115 120 125
Leu Asn Leu Gln Arg Ala Ser Thr Thr Thr His Arg Thr Ala Thr Thr
130 135 140
Thr Thr Arg Arg Thr Thr Thr Ser Pro Thr Thr Arg Gln Met
145 150 155 160
Thr Thr Thr Pro Ala Ala Leu Pro Thr Thr Val Val Thr Thr Pro Asp
165 170 175
Leu Thr Thr Gly Thr Pro Leu Gln Met Thr Thr Ile Ala Val Phe Thr
180 185 190
Thr Ala Asn Thr Cys Leu Ser Leu Thr Pro Ser Thr Leu Pro Glu Glu
195 200 205
Ala Thr Gly Leu Leu Thr Pro Glu Pro Ser Lys Glu Gly Pro Ile Leu
210 215 220
Thr Ala Glu Ser Glu Thr Val Leu Pro Ser Asp Ser Trp Ser Ser Ala
225 230 235 240
Glu Ser Thr Ser Ala Asp Thr Val Leu Leu Thr Ser Lys Glu Ser Lys
245 250 255
Val Trp Asp Leu Pro Ser Thr Ser His Val Ser Met Trp Lys Thr Ser
260 265 270
Asp Ser Val Ser Ser Pro Gln Pro Gly Ala Ser Asp Thr Ala Val Pro
275 280 285
Glu Gln Asn Lys Thr Thr Lys Thr Gly Gln Met Asp Gly Ile Pro Met
290 295 300
Ser Met Lys Asn Glu Met Pro Ile Ser Gln Leu Leu Met Ile Ile Ala
305 310 315 320
Pro Ser Leu Gly Phe Val Leu Phe Ala Leu Phe Val Ala Phe Leu Leu
325 330 335
Arg Gly Lys Leu Met Glu Thr Tyr Cys Ser Gln Lys His Thr Arg Leu
340 345 350
Asp Tyr Ile Gly Asp Ser Lys Asn Val Leu Asn Asp Val Gln His Gly
355 360 365
Arg Glu Asp Glu Asp Gly Leu Phe Thr Leu
370 375

<210> 34
<211> 1156
<212> DNA

Seqlist_12_20_06.txt

<213> H. sapiens

<400> 34

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ctgtactcat cctggctca caacagcaac agcatgtgct gggggaaaaga ccagtcccc 180
tactccgggtt gcaaggaggc gctcatccgc actgatggaa tgagggtgac ctcagaaaag 240
tcagaaaaat atagacttca ggggactatc ccgagaggtg atgttcctt gaccatctta 300
aaccccaagt aaagtgacag cggtgtgtac tgctgcccga tagaagtgcc tggctggttc 360
aacatgtaa agataaacgt gcgcctgaat ctacagagag cctcaacaac cacgcacaga 420
acagcaacca ccaccacacg cagaacaaca acaacaaggc ccaccaccac ccgacaaatg 480
acaacaaccc cagctgact tccaacaaca gtcgtgacca caccgatct cacaaccgga 540
acaccactcc agatgacaac cattggcgtc ttcacaacag caaacacgtg ccttcacta 600
accccaagca cccttccgga ggaagccaca ggtcttctga ctcccggagcc ttctaaggaa 660
gggcccattcc tcaactgcaga atcagaaaact gtcctccca gtgattccctg gagtagtgc 720
gagtctactt ctgctgacac tgcctgctg acatccaaag agtccaaagt ttggatctc 780
ccatcaacat cccacgtgtc aatgtggaaa acgagtgtt ctgtgtctt tcctcagcct 840
ggagcatctg atacagcagt tcctgagcag aaaaaacaaa caaaaacagg acagatggat 900
ggaataccca tgtcaatgaa gaatgaaaatg cccatctccc aactactgat gatcatcgcc 960
ccctccttgg gatttgtgct cttcgattt gttgtggcgt ttctcctgag agggaaactc 1020
atggaaacactt attgttcgca gaaacacaca aggctagact acattggaga tagaaaaat 1080
gtcctcaatg acgtgcagca tggaaaggaa gacgaagacg gccttttac cctctaacaa 1140
cgcagtagca tggtag 1156

<210> 35

<211> 378

<212> PRT

<213> H. sapiens

<220>

<221> VARIANT

<222> (1)...(378)

<223> TIM-4, allele 2

<400> 35

Met Ser Lys Glu Pro Leu Ile Leu Trp Leu Met Ile Glu Phe Trp Trp
1 5 10 15
Leu Tyr Leu Thr Pro Val Thr Ser Glu Thr Val Val Thr Glu Val Leu
20 25 30
Gly His Arg Val Thr Leu Pro Cys Leu Tyr Ser Ser Trp Ser His Asn
35 40 45
Ser Asn Ser Met Cys Trp Gly Lys Asp Gln Cys Pro Tyr Ser Gly Cys
50 55 60
Lys Glu Ala Leu Ile Arg Thr Asp Gly Met Arg Val Thr Ser Arg Lys
65 70 75 80
Ser Ala Lys Tyr Arg Leu Gln Gly Thr Ile Pro Arg Gly Asp Val Ser
85 90 95
Leu Thr Ile Leu Asn Pro Ser Glu Ser Asp Ser Gly Val Tyr Cys Cys
100 105 110
Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Ile Asn Val Arg
115 120 125
Leu Asn Leu Gln Arg Ala Ser Thr Thr His Arg Thr Ala Thr Thr
130 135 140
Thr Thr Arg Arg Thr Thr Ser Pro Thr Thr Arg Gln Met
145 150 155 160
Thr Thr Thr Pro Ala Ala Leu Pro Thr Thr Val Val Thr Thr Pro Asp
165 170 175
Leu Thr Thr Gly Thr Pro Leu Gln Met Thr Thr Ile Ala Val Phe Thr
180 185 190
Thr Ala Asn Thr Cys Leu Ser Leu Thr Pro Ser Thr Leu Pro Glu Glu
195 200 205
Ala Thr Gly Leu Leu Thr Pro Glu Pro Ser Lys Glu Gly Pro Ile Leu
210 215 220

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Thr	Ala	Glu	Ser	Glu	Thr	Val	Leu	Pro	Ser	Asp	Ser	Trp	Ser	Ser	Val
225				230				235							240
Glu	Ser	Thr	Ser	Ala	Asp	Thr	Val	Leu	Leu	Thr	Ser	Lys	Glu	Ser	Lys
				245				250							255
val	Trp	Asp	Leu	Pro	Ser	Thr	Ser	His	Val	Ser	Met	Trp	Lys	Thr	Ser
				260				265							270
Asp	Ser	Val	Ser	Ser	Pro	Gln	Pro	Gly	Ala	Ser	Asp	Thr	Ala	Val	Pro
				275				280							285
Glu	Gln	Asn	Lys	Thr	Thr	Lys	Thr	Gly	Gln	Met	Asp	Gly	Ile	Pro	Met
				290				295							300
Ser	Met	Lys	Asn	Glu	Met	Pro	Ile	Ser	Gln	Leu	Leu	Met	Ile	Ile	Ala
					310					315					320
Pro	Ser	Leu	Gly	Phe	Val	Leu	Phe	Ala	Leu	Phe	Val	Ala	Phe	Leu	Leu
				325				330							335
Arg	Gly	Lys	Leu	Met	Glu	Thr	Tyr	Cys	Ser	Gln	Lys	His	Thr	Arg	Leu
				340				345							350
Asp	Tyr	Ile	Gly	Asp	Ser	Lys	Asn	Val	Leu	Asn	Asp	Val	Gln	His	Gly
				355				360							365
Arg	Glu	Asp	Glu	Asp	Gly	Leu	Phe	Thr	Leu						
				370				375							

<210> 36
<211> 1156
<212> DNA
<213> H. sapiens

<400> 36
atgtccaaag aacctctcat tctctggctg atgattgagt tttgggtggct ttacctgaca 60
ccagtcactt cagagactgt tgtgacggag gttttgggtc accggggtgac ttggccctgt 120
ctgtactcat cctggctctca caacagcaac agcatgtgct gggggaaaaga ccagtgc(ccc 180
tactccggtt gcaaggaggc gctcatccgc actgatggaa tgagggtgac ctcaagaaag 240
tcagcaaaat atagacttca ggggactatc ccgagagggt atgtctccctt gaccatctta 300
aaccccagtg aagaatgacac cggtgtgtac tgctgcccga tagaagtgtcc tggctggttc 360
aacatgttaa agataaaacgt gcgccttgaat ctacagagag cctcaacaac cacgcacaga 420
acagcaacca ccaccacacg cagaacaaca acaacaagcc ccaccaccac ccgacaaatg 480
acaacaaccc cagctgact tccaacaaca gtcgtgacca caccggatct cacaaccgga 540
acaccactcc agatgacaac cattggcgac ttcacaacag caaacacgtg cttttcaacta 600
accccaagca cccttccgga ggaagccaca ggtttcttga ctccccgagcc ttctaaggaa 660
gggccccatcc tcactgcaga atcagaaaact gtcctcccca gtgattcctg gagtagtgtt 720
gagtctactt ctgctgacac tgccttgctg acatccaaag agtccaaagt ttggatctc 780
ccatcaacat cccacgtgtc aatgtggaaa acgagtgtatt ctgtgtcttc tcctcagcct 840
ggagcatctg atacagcagt tcctgagcag aaaaaaccaa aaaaaacagg acagatggat 900
ggaataccca tgtcaatgaa gaatgaaatg cccatctccc aactactgtat gatcatcgcc 960
ccctcccttg gatttgtgtc cttcgattt gttgtggcgt ttctccctgag agggaaaactc 1020
atggaaacactt atgttgcga gaaacacaca aggctagact acattggaga tagaaaaat 1080
gtcctcaatg acgtgcagca tggaaaggaa gacgaagacg gccttttac cctctaacaa 1140
cgcagtagca tgttag 1156

<210> 37
<211> 481
<212> DNA
<213> H. sapiens

<220>
<221> exon
<222> (152)...(430)
<223> Exon 3, reference sequence

<400> 37
ttctagctgg gcaatgacca agattgacag ttcaggaagt taactccacc tagggacagt 60
ctgtcattgg tgtgcttaggg tacagttcca gcctgaggtt cttgtttctt gtttgactta 120
tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180

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actgttccaa ccgtcacgac tgttcaacg agcaccactg ttccaacgac aacgactgtt 240
ccaacgacaa ctgttccaac aacaatgagc attccaacga caacgactgt tctgacgaca 300
atgactgtt caacgacaac gagcgttcca acgacaacga gcattccaac aacaacaagt 360
gttccagtga caacaactgt ctctaccttt gttcctccaa tgccttgcc caggcagaac 420
catgaaccag gtaaaaacaga tgtgttggg agccccaaagg ccttctaattg aggagctg 480
g 481

<210> 38
<211> 499
<212> DNA
<213> H. sapiens

<220>
<221> exon
<222> (152)...(448)
<223> Exon 3, INS157 polymorphism

<400> 38
ttcttagctgg gcaatgacca agattgacag ttccaggaagt taactccacc tagggacagt 60
ctgtcattgg tttgtcttaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
actgttccaa ccgtcacgac tgttcaacg agcaccactg ttccaacgac aacgactgtt 240
ccaatgacaa cgactgttcc aacgacaact gttccaacaa caatgagcat tccaacgaca 300
acgactgttc tgacgacaat gactgttca acgacaacga gcgttccaac gacaacgagc 360
attccaacaa caacaagtgt tccagtgaca acaactgtct ctacctttgt tcctccaatg 420
cctttggccca ggcagaacca tgaaccaggtaaaa acagatgtgt tggttggaaag cccaaaggccc 480
ttctaattgag gagctgcgg 499

<210> 39
<211> 496
<212> DNA
<213> H. sapiens

<220>
<221> exon
<222> (152)...(445)
<223> Exon 3, 195delT polymorphism

<400> 39
ttcttagctgg gcaatgacca agattgacag ttccaggaagt taactccacc tagggacagt 60
ctgtcattgg tttgtcttaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180
actgttccaa ccgtcacgac tgttcaacg agcaccactg ttccaacgac aacgactgtt 240
ccaatgacaa cgactgttcc aacgacaact gttccaacaa caatgagcat tccaacgaca 300
acgactgttc tgacgacaat gactgttca acgacaacga gcgttccaac gacaacgagc 360
attccaacaa caagtgttcc agtgacaaca actgtctcta cctttgttcc tccaatgcct 420
ttggccaggc agaaccatgaa accaggtaaa acagatgtgt ttggaaagccc aaaggccttc 480
taatgaggag ctgcgg 496

<210> 40
<211> 496
<212> DNA
<213> H. sapiens

<220>
<221> exon
<222> (152)...(445)
<223> Exon 3, 157insMTTVP polymorphism

<400> 40
ttcttagctgg gcaatgacca agattgacag ttccaggaagt taactccacc tagggacagt 60
ctgtcattgg tttgtcttaggg tacagttcca gcctgaggct cttgtttctt gtttgactta 120
tgctcactct catgttgatt tctgactcca gccaaaggta cgactactcc aattgtcaca 180

Seqlist_12_20_06.txt

actgttccaa ccgtcacgac tgttcaaacg agcaccactg ttccaacgac aacgactgtt 240
ccaatgacga ctgttccaaac gacaactgtt ccaacaacaa tgagcattcc aacgacaacg 300
actgttctga cgacaatgac tgttcaaacg acaacgagcg ttccaacgac aacgagcatt 360
ccaacaacaa caagtgttcc agtgacaaca actgtctcta cctttgttcc tccaatgcct 420
ttgcccaggc agaaccatga accaggtaaa acagatgtgt ttggaaagccc aaaggccttc 480
taatgaggag ctgcgg 496

<210> 41
<211> 18
<212> DNA
<213> H. sapiens

<400> 41
gtgtctgaca gtggcgta 18

<210> 42
<211> 18
<212> DNA
<213> H. sapiens

<400> 42
tttgcccagg cagaacca 18

<210> 43
<211> 18
<212> DNA
<213> H. sapiens

<400> 43
ccacccaagg tcacgact 18

<210> 44
<211> 18
<212> DNA
<213> H. sapiens

<400> 44
atgccacgga ctaagacc 18

<210> 45
<211> 41
<212> DNA
<213> H. sapiens

<400> 45
ggaattcgtc gaccaccatg catcctcaag tggtcatctt a 41

<210> 46
<211> 42
<212> DNA
<213> H. sapiens

<400> 46
ggaattcgtcg gccgctcatt agtccgtggc ataaacagta tt 42

<210> 47
<211> 20
<212> DNA
<213> H. sapiens

<400> 47
tcaagtggtc atcttaagcc 20

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<210> 48
<211> 22
<212> DNA
<213> H. sapiens

<400> 48
taaactctca aagagcacca ct 22

<210> 49
<211> 22
<212> DNA
<213> H. sapiens

<400> 49
acagactcca gcatagattc ct 22

<210> 50
<211> 22
<212> DNA
<213> H. sapiens

<400> 50
gcaccaagac agaaatacag ac 22

<210> 51
<211> 31
<212> DNA
<213> H. sapiens

<400> 51
agaagcaccc aagacagaaa tacagactcc a 31

<210> 52
<211> 19
<212> DNA
<213> H. sapiens

<400> 52
ttcttagctgg gcaatgacc 19

<210> 53
<211> 20
<212> DNA
<213> H. sapiens

<400> 53
ccgcagctcc tcattagaag 20

<210> 54
<211> 307
<212> PRT
<213> rattus norvegicus

<400> 54
Met Val Gln Leu Gln Val Phe Ile Ser Gly Leu Leu Leu Leu Pro
1 5 10 15
Gly Ser Val Asp Ser Tyr Glu Val Val Lys Gly Val Val Gly His Pro
20 25 30
Val Thr Ile Pro Cys Thr Tyr Ser Thr Arg Gly Gly Ile Thr Thr Thr
35 40 45
Cys Trp Gly Arg Gly Gln Cys Pro Tyr Ser Ser Cys Gln Asn Ile Leu

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50	55	60
Ile Trp Thr Asn Gly Tyr Gln Val Thr Tyr Arg Ser Ser Gly Arg Tyr	65	70
Asn Ile Lys Gly Arg Ile Ser Glu Gly Asp Val Ser Leu Thr Ile Glu	75	80
Asn Ser Val Asp Ser Asp Ser Gly Leu Tyr Cys Cys Arg Val Glu Ile	85	90
Pro Gly Trp Phe Asn Asp Gln Lys Met Thr Phe Ser Leu Glu Val Lys	100	105
Pro Glu Ile Pro Thr Ser Pro Pro Thr Arg Pro Thr Thr Thr Arg Pro	115	120
Thr Thr Thr Arg Pro Thr Thr Ile Ser Thr Arg Ser Thr His Val Pro	130	135
Thr Ser Thr Arg Val Ser Thr Ser Thr Pro Thr Pro Glu Gln Thr Gln	145	150
Thr His Lys Pro Glu Ile Thr Thr Phe Tyr Ala His Glu Thr Thr Ala	165	170
Glu Val Thr Glu Thr Pro Ser Tyr Thr Pro Ala Asp Trp Asn Gly Thr	180	185
Val Thr Ser Ser Glu Glu Ala Trp Asn Asn His Thr Val Arg Ile Pro	195	200
Leu Arg Lys Pro Gln Arg Asn Pro Thr Lys Gly Phe Tyr Val Gly Met	210	215
Ser Val Ala Ala Leu Leu Leu Leu Leu Ala Ser Thr Val Val Val	225	230
Thr Arg Tyr Ile Ile Arg Lys Lys Met Gly Ser Leu Ser Phe Val	245	250
Ala Phe His Val Ser Lys Ser Arg Ala Leu Gln Asn Ala Ala Ile Val	260	265
His Pro Arg Ala Glu Asp Asn Ile Tyr Ile Ile Glu Asp Arg Ser Arg	275	280
Gly Ala Glu	290	295
	305	300

<210> 55

<211> 451

<212> PRT

<213> Chlorocebus aethiops

<400> 55

1	5	10
Met His Leu Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp	15	15
Ser Val Ala Asp Ser Val Asn Val Asp Gly Val Ala Gly Leu Ser Ile	20	25
Thr Leu Pro Cys Arg Tyr Asn Gly Ala Ile Thr Ser Met Cys Trp Asn	30	35
Arg Gly Thr Cys Ser Val Phe Ser Cys Pro Asp Gly Ile Val Trp Thr	40	45
Asn Gly Thr His Val Thr Tyr Arg Lys Glu Thr Arg Tyr Lys Leu Leu	50	55
Gly Asn Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Ala Asn Thr Ala	60	65
Val Ser Asp Ser Gly Ile Tyr Cys Cys Arg Val Lys His Ser Gly Trp	70	75
Phe Asn Asp Met Lys Ile Thr Ile Ser Leu Lys Ile Gly Pro Pro Arg	80	85
Val Thr Thr Pro Ile Val Arg Thr Val Arg Thr Ser Thr Thr Val Pro	95	100
Thr Thr Thr Thr Leu Pro Thr Thr Thr Thr Leu Pro Thr Thr Thr Thr	110	115
Leu Pro Thr Thr Thr Thr Leu Pro Met Thr Thr Thr Leu Pro Met Thr	125	130
Thr Thr Leu Pro Thr Thr Thr Val Pro Thr Thr Thr Thr Leu Pro	140	145
	150	155
	160	165
	170	175
	175	180

Seqlist_12_20_06.txt

<210> 56
<211> 359
<212> PRT
<213> *H. sapiens*

<400> 56
 Met His Pro Gln Val Val Ile Leu Ser Leu Ile Leu His Leu Ala Asp
 1 5 10 15
 Ser Val Ala Gly Ser Val Lys Val Gly Gly Glu Ala Gly Pro Ser Val
 20 25 30
 Thr Leu Pro Cys His Tyr Ser Gly Ala Val Thr Ser Met Cys Trp Asn
 35 40 45
 Arg Gly Ser Cys Ser Leu Phe Thr Cys Gln Asn Gly Ile Val Trp Thr
 50 55 60
 Asn Gly Thr His Val Thr Tyr Arg Lys Asp Thr Arg Tyr Lys Leu Leu
 65 70 75 80
 Gly Asp Leu Ser Arg Arg Asp Val Ser Leu Thr Ile Glu Asn Thr Ala
 85 90 95
 Val Ser Asp Ser Gly Val Tyr Cys Cys Arg Val Glu His Arg Gly Trp
 100 105 110
 Phe Asn Asp Met Lys Ile Thr Val Ser Leu Glu Ile Val Pro Pro Lys
 115 120 125
 Val Thr Thr Thr Pro Ile Val Thr Thr Val Pro Thr Val Thr Thr Val
 130 135 140
 Arg Thr Ser Thr Thr Val Pro Thr Thr Thr Val Pro Thr Thr Thr
 145 150 155 160

Seqlist_12_20_06.txt

Val Pro Thr Thr Met Ser Ile Pro Thr Thr Thr Thr Val Pro Thr Thr
165 170 175
Met Thr Val Ser Thr Thr Thr Ser Val Pro Thr Thr Thr Ser Ile Pro
180 185 190
Thr Thr Thr Ser Val Pro Val Thr Thr Thr Val Ser Thr Phe Val Pro
195 200 205
Pro Met Pro Leu Pro Arg Gln Asn His Glu Pro Val Ala Thr Ser Pro
210 215 220
Ser Ser Pro Gln Pro Ala Glu Thr His Pro Thr Thr Leu Gln Gly Ala
225 230 235 240
Ile Arg Arg Glu Pro Thr Ser Ser Pro Leu Tyr Ser Tyr Thr Thr Asp
245 250 255
Gly Asn Asp Thr Val Thr Glu Ser Ser Asp Gly Leu Trp Asn Asn Asn
260 265 270
Gln Thr Gln Leu Phe Leu Glu His Ser Leu Leu Thr Ala Asn Thr Thr
275 280 285
Lys Gly Ile Tyr Ala Gly Val Cys Ile Ser Val Leu Val Leu Leu Ala
290 295 300
Leu Leu Gly Val Ile Ile Ala Lys Lys Tyr Phe Phe Lys Lys Glu Val
305 310 315 320
Gln Gln Leu Ser Val Ser Phe Ser Ser Leu Gln Ile Lys Ala Leu Gln
325 330 335
Asn Ala Val Glu Lys Glu Val Gln Ala Glu Asp Asn Ile Tyr Ile Glu
340 345 350
Asn Ser Leu Tyr Ala Thr Asp
355

<210> 57
<211> 6
<212> PRT
<213> H. sapiens

<400> 57
Met Thr Thr Thr Val Pro
1 5

<210> 58
<211> 7
<212> PRT
<213> H. sapiens

<400> 58
Ser Val Val Tyr Gly Leu Arg
1 5